



File Copy
09/671,687
updated

STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 09/671,687

TO: David Lamberston
Location: rem/2b79/2c70
Art Unit: 1636
Tuesday, April 19, 2005

Case Serial Number: 09/671687

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Lamberston,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



STIC-Biotech/ChemLib**150771** *mj*SEARCHED
PPR 15 2005SEARCHED
(STIC)

From: Lambertson, David
Sent: Friday, April 15, 2005 10:25 AM
To: STIC-Biotech/ChemLib
Cc: Lambertson, David
Subject: Search Request

Search Request

Examiner's Name:	David Lambertson
Examiner #:	79514
Art Unit:	1636
Room #:	02B79 Remsen
Mailbox room#:	02C70 Remsen
Phone:	(571) 272-0771
Results Format:	paper

Serial #:09/671687**Please Search:****Protein and Nucleic Acid databases for:****SEQ ID No: 3****Including:**

1. Default Search.
2. Oligomer Search.
3. Interference Search.

Thanks,
Dave.

*4/15/05
AA → AA
AA → NR
OBP*

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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:14:54 ; Search time 73 Seconds

(without alignments)

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: GeneseqP1980:*

2: GeneseqP1990:*

3: GeneseqP2000B:*

4: GeneseqP2001B:*

5: GeneseqP2002B:*

6: GeneseqP2003As:*

7: GeneseqP2003Bs:*

8: GeneseqP2004S:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

Title:	US-09-671-687A-3
Perfect score:	5034
Sequence:	1 M ^S G ^L M ^S Q ^B K ^V T ^S P ^Y W ^E R ^IR ^L C ^D A ^M C ^M Y ^S P ^T M ^L Y ^K 949
Scoring table:	BLOSUM62
Gapop:	10.0 , Gapext 0.5
Searched:	2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters:	2105692

RESULT 1

ADC24816

ID ADC24816 standard; protein; 953 AA.

XX

AC ADC24816;

XX

DT 18-DEC-2003 (first entry)

XX

DB Human breast specific polypeptide (BSP) DEX0238_137, SEQ ID NO:137.

XX

Human; breast specific polypeptide; BSP; breast specific nucleic acid; BSNA; breast cancer; metastasis; non-cancerous disease; breast tissue; identification; monitoring; diagnosis; engineered breast tissue production; transgenic animal; cytostatic; gene therapy; vaccine; chromosome 16p13.3.; drug screening; Homo sapiens.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	4.983	99.0	953	7	ADC24816	Adc24816 Human breast specific polypeptide (BSP) DEX0238_137, SEQ ID NO:137.
2	4.983	99.0	953	8	ADQ95916	Adq95916 Human T cell ac
3	4.983	99.0	960	8	ADR99244	Adr99244 DKFZ0586D
4	4.980	98.9	953	8	ADQ95916	Adq95916 T cell ac
5	4.971.5	98.8	956	6	ABB82783	Abb82783 Human CYL
6	4.971.5	98.8	956	8	ADR14489	Adr14489 Human NP-
7	4.968	98.7	956	8	ADQ95920	Adq95920 T cell ac
8	3.876.5	77.0	739	4	Aau23747	Aau23747 Novel human breast specific polypeptide (BSP) DEX0238_137, SEQ ID NO:137.
9	3.862	76.7	731	3	AAV91954	AAV91954 Human cyt
10	3.855	76.6	731	4	ABP95828	Abp95828 Human pro
11	3.636	72.2	685	4	AMM39254	Amm39254 Human pol
12	3.553	70.8	698	4	AAM41040	Aam41040 Human pol
13	2.755	54.7	558	4	AAU23211	Aau23211 Novel human breast specific polypeptide (BSP) DEX0238_137, SEQ ID NO:137.
14	2.343	46.5	476	4	AAB95719	Aab95719 Human pro
15	1.225	25.3	261	5	ABB89233	Abb89233 Human pol
16	1.173	23.3	238	5	ABB89234	Abb89234 Human pol
17	0.856	17.0	517	4	ABB61656	Abb61656 Drosophila
18	0.597	11.9	113	4	AAM14365	Aam14365 Peptide #
19	0.597	11.9	113	4	ABB333941	Abb333941 Peptide #
20	0.597	11.9	113	4	AAM27399	Aam27399 Peptide #
21	0.597	11.9	113	4	ABB28754	Abb28754 Peptide #
22	0.597	11.9	113	4	ABB19577	Abb19577 Protein #
23	0.597	11.9	113	4	AAM67104	Aam67104 Human bone
24	0.597	11.9	113	4	AAM54704	Aam54704 Human brain
25	0.597	11.9	113	4	AAM02691	Aam02691 Peptide #

The invention relates to breast specific polypeptides (BSPs) and nucleic acids (breast specific nucleic acids; BSNA) encoding them. The invention also relates to vectors and host cells comprising a DNA sequence;

antibodies against BSPs; the recombinant production of BSPs; methods of detection of BSNA or BSPs in a sample; kits for detecting a risk of

cancer or presence of cancer in a patient; and vaccines comprising a BSNA or BSP. The invention additionally discloses fragments, mutants, fusion proteins, homologous proteins and allelic variants of BSPs; methods for identifying and designing agonists and antagonists of BSPs; methods for

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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:25:00 ; Search time 97 Seconds
(without alignments)

Scoring table: BLOSUM62

Title: US-09-671-687A-3

Perfect score: 5034 seqs, 332370683 residues

Sequence: 1 MSSGLMSQEKVTSPIVEERI.....RLCDAYMCMYQSPMTMSLYK 949

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Post-processing: Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
 1: /cgn2_6_ptodata/1/pubpaas/us07_PUBCOMB.pep:
 2: /cgn2_6_ptodata/1/pubpaas/us07_PUBCOMB.pep:
 3: /cgn2_6_ptodata/1/pubpaas/us07_PUBCOMB.pep:
 4: /cgn2_6_ptodata/1/pubpaas/us07_PUBCOMB.pep:
 5: /cgn2_6_ptodata/1/pubpaas/us07_PUBCOMB.pep:
 6: /cgn2_6_ptodata/1/pubpaas/us07_PUBCOMB.pep:
 7: /cgn2_6_ptodata/1/pubpaas/us07_PUBCOMB.pep:
 8: /cgn2_6_ptodata/1/pubpaas/us08_PUBCOMB.pep:
 9: /cgn2_6_ptodata/1/pubpaas/us08_PUBCOMB.pep:
 10: /cgn2_6_ptodata/1/pubpaas/us08_PUBCOMB.pep:
 11: /cgn2_6_ptodata/1/pubpaas/us09_PUBCOMB.pep:
 12: /cgn2_6_ptodata/1/pubpaas/us09_NIN_PUB.pep:
 13: /cgn2_6_ptodata/1/pubpaas/us10_PUBCOMB.pep:
 14: /cgn2_6_ptodata/1/pubpaas/us10_PUBCOMB.pep:
 15: /cgn2_6_ptodata/1/pubpaas/us10_PUBCOMB.pep:
 16: /cgn2_6_ptodata/1/pubpaas/us10_NIN_PUB.pep:
 17: /cgn2_6_ptodata/1/pubpaas/us10_NIN_PUB.pep:
 18: /cgn2_6_ptodata/1/pubpaas/us11_NIN_PUB.pep:
 19: /cgn2_6_ptodata/1/pubpaas/us60_NIN_PUB.pep:
 20: /cgn2_6_ptodata/1/pubpaas/us60_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	4983	99.0	960	16	US-10-788-792-250	Sequence 250, App
2	4971.5	98.8	956	10	US-09-764-868-731	Sequence 251, App
3	4971.5	98.8	956	16	US-10-437-963-132799	Sequence 252, App
4	3862	76.7	731	16	US-10-698-5606	Sequence 253, App
5	1275	25.3	261	15	US-10-264-237-1609	Sequence 254, App
6	1173	23.3	238	15	US-10-264-237-1610	Sequence 255, App
7	597	11.9	113	9	US-09-864-761-34675	Sequence 256, A
8	146	2.9	354	13	US-10-087-192-120	Sequence 257, App
9	143	2.8	547	15	US-10-108-260A-2751	Sequence 258, App
10	143	2.8	547	15	US-10-275-595A-13	Sequence 259, App
11	135.5	2.7	306	15	US-10-104-047-990	Sequence 260, App
12	135.5	2.7	721	11	US-09-764-875-957	Sequence 261, App
13	135.5	2.7	2273	15	US-10-282-122A-6615	Sequence 262, A

ALIGMENTS

RESULT 1

US-10-788-792-250

Sequence 251, Application US-10-788-792

Publication No. US20040191819A1

GENERAL INFORMATION:

APPLICANT: Bayer Pharmaceuticals Corporation

APPLICANT: Eveleigh, Deepa

APPLICANT: Bigwood, Douglas

TITLE OF INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF USE

FILE REFERENCE: 5152

CURRENT APPLICATION NUMBER: US-10-788-792

PRIOR APPLICATION NUMBER: US-10-425-114-72939

PRIOR FILING DATE: 2004-02-27

NUMBER OF SEQ ID NOS: 254

SEQ ID NO 250

TYPE: PRT

ORGANISM: Homo sapiens

US-10-788-792-250

Query Match 99.0%; Score 4983; DB 16; Length 960;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 948; Conservatve 0; Mismatches 1; Indels 4; Gaps 4;

Qy 1 MSSGMWSQKVTSPWEEFYLQECVTDQKQLJKVPKCSIGQTQDRSGHSHR 60

Db 8 MSSGMWSQKVTSPWEEFYLQECVTDQKQLJKVPKCSIGQTQDRSGHSHR 67

Qy 61 PSAKKKKQIGKIKLQEPAHLFDE-DVVEINEKFTELLATINCEERFLSFNQRNL 119

Db 68 PSAKKKKQIGKIKLQEPAHLFDE-DVVEINEKFTELLATINCEERFLSFNQRNL 127

Qy 120 KGLQDVGCPVKYQIQLRSGBEKKPFPVVRFRGPLLARTYGGPPVTELLEGRGCGPTDCV 179

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_P2n model

Run on: April 18, 2005, 15:26:40 ; Search time 8972 Seconds

(without alignments)

5125.279 Million cell updates/sec

Title: US-09-671-687A-3

Perfect score: 5034

Sequence: 1 MSSGMWSQEKVTSPTWEERI.....RLLCDAYMCMYQSPTMSLYK 949

Scoring table: BL051662

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0‡

Maximum Match 100‡

Listing first 45 summaries

Command line parameters:

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-MDBL=frame_p2n.model -DBXaxP
-Q/-cgn2.1/-USPTO spool/p/US09671687/runat_18042005_115018_17125/app_query.fasta_1.1.095
-DEF=GenBank1 -QFMT=fasta -SUFFIX=erg -MINMATCH=0.1 -QOPCT=0 -LOOPET=0
-UNITS=bits -START=1 -END=1 -MATRIX=blobune62 -TRANS=human40.cgi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGNN=15 -MODE=LOCAL
-OUTFMT=PT0 -HEAPSIZE=60 -MINLEN=0 -MAXLEN=2000000000
-USBR=US09671687.0CGN_1.1_5312@runat_18042005_115018_17125 -RCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -TREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6
```

Database : GenEmbl:*

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1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	4983	99.0	CQ834224	
2	4983	99.0	BC012342	Sequence
3	4983	99.0	AB02656	Homo sapi
4	4980	98.9	CQ834222	Sequence

ALIGMENTS
RESULT 1
CQ834224
LOCUS CQ834224 Sequence 95 from Patent WO2004058805.
DEFINITION CQ834224
ACCESSION CQ834224.1 GI:50833761
VERSION
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Matsuda, A. and Yoneca, S.
TITLE T cell activating gene
JOURNAL Patent: WO 2004058805-A 95 15-JUL-2004;
FEATURES Location/Qualifier
Source 1 .. 3302
CDS
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="unnamed protein product"
/codon_start=1
243 .. 3104

Result No.	Query	Score	Match length	DB ID	Description
1	/cgcn2_6/.ptodata/1/ina/5A.COMB.seq:*	3676	73.0	2523	US-09-620-312D-290 Sequence 290, APP Sequence 3, Appl
2	/cgcn2_6/.ptodata/1/ina/5B.COMB.seq:*	2468	49.0	2116	US-09-646-403-3 Sequence 20085, A Sequence 79, Appl
3	/cgcn2_6/.ptodata/1/ina/6A.COMB.seq:*	185	3.7	110	US-09-513-999C-20085 Sequence 189, AP Sequence 5779, AP Sequence 56, Appl
4	/cgcn2_6/.ptodata/1/ina/6B.COMB.seq:*	151	3.0	5857	US-09-220-132-79 Sequence 189, AP Sequence 5779, AP Sequence 56, Appl
5	/cgcn2_6/.ptodata/1/ina/PCUTS.COMB.seq:*	139	2.8	2825	US-09-949-016-1895 Sequence 10072, A Sequence 57, Appl
6	/cgcn2_6/.ptodata/1/ina/backfles1.seq:*	139	2.8	3100	US-09-949-016-5779 Sequence 10072, A Sequence 57, Appl
7	/cgcn2_6/.ptodata/1/ina/backfles1.seq:*	135	2.7	2643	US-09-399-913-56 Sequence 352, APP Sequence 10072, A Sequence 57, Appl
8	/cgcn2_6/.ptodata/1/ina/5A.COMB.seq:*	135	2.7	2643	US-09-350-614-56 Sequence 352, APP Sequence 10072, A Sequence 57, Appl
9	/cgcn2_6/.ptodata/1/ina/5B.COMB.seq:*	133	2.6	3245	US-09-744-528-152 Sequence 352, APP Sequence 10072, A Sequence 57, Appl
10	/cgcn2_6/.ptodata/1/ina/6A.COMB.seq:*	130	2.6	1452	US-09-248-796A-10072 Sequence 352, APP Sequence 10072, A Sequence 57, Appl
11	/cgcn2_6/.ptodata/1/ina/6B.COMB.seq:*	128	2.6	5610	US-09-262-537-57 Sequence 352, APP Sequence 10072, A Sequence 57, Appl
12	/cgcn2_6/.ptodata/1/ina/PCUTS.COMB.seq:*	126	2.5	1503	US-08-999-774A-11 Sequence 11, Appl

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		Result No.	Score	Query Match Length DB ID	Description
OM protein - nucleic search, using frame_plus_p2n model		1 : 4971.5	98.8	5371 10 US-09-851-673-3	Sequence 3, Appli
Run on: April 18, 2005, 18:28:51 ; Search time 1146 Seconds (without alignments)		2 : 4971.5	98.8	5371 18 US-10-755-889-489	Sequence 489, App
Perfect score: 5034		3 : 4942	98.2	4527 18 US-10-921-707-154	Sequence 250, App
Sequence: 1 MSSGLSQBKVTSPYNEBRI.....RLLCDAYMCMYQSPINTNSLYK 949		4 : 3676	73.0	2523 15 US-10-037-270-290	Sequence 290, App
Scoring table: BLOSUM62		5 : 3676	73.0	2523 17 US-10-117-722-290	Sequence 3, Appli
Xgapop 10.0 ; Xgapext 0.5		6 : 2468	49.0	2116 18 US-10-761-370-3	Sequence 204, App
Ygapop 10.0 ; Ygapext 0.5		c : 1778	35.3	1151 17 US-10-264-237-204	Sequence 05, App
Fgapop 6.0 ; Fgapext 7.0		c : 1494	29.7	1013 17 US-10-264-237-205	Sequence 4253, App
Delopt 6.0 ; Delext 7.0		c : 1102	21.9	617 11 US-09-969-034-4253	Sequence 4254, App
Searched:		c : 10	879	17.5	557 11 US-09-969-034-4254
BLOSUM62 seqs, 3033355566 residues		c : 11	626	12.4	376 9 US-09-983-965-1633
Total number of hits satisfying chosen parameters:	11245032	c : 12	545	10.8	309 9 US-09-864-761-1845
Minimum DB seq length: 0		c : 13	512	10.2	483 9 US-09-864-761-1386
Maximum DB seq length: 2000000000		c : 14	412	8.2	425 10 US-09-918-995-25878
Post-processing: Minimum Match 0% ; Maximum Match 100% ; Listing First 45 summaries		c : 15	160.5	3.2	4847 17 US-10-152-319A-1764
		c : 16	151	3.0	5857 10 US-09-873-367C-305
		c : 17	151	3.0	5857 19 US-10-843-641A-305
		c : 18	148	2.9	3051 17 US-10-371-905A-13
		c : 19	146	2.9	1380 13 US-10-087-192-119
		c : 20	146	2.9	5563 18 US-10-723-60-1545
		c : 21	146	2.9	5607 18 US-10-723-860-5973
		c : 22	143	2.8	3287 17 US-10-275-595A-47
		c : 23	143	2.8	3370 17 US-10-108-260A-308
		c : 24	143	2.8	3592 10 US-09-814-353-2078
		c : 25	138	2.7	2154 17 US-10-369-493-45974
		c : 26	138	2.7	2451 18 US-10-437-13-30316
		c : 27	136.5	2.7	3409 18 US-10-108-260A-308
		c : 28	135.5	2.7	2618 17 US-10-104-047-1020
		c : 29	135.5	2.7	3103 11 US-09-764-75-259
		c : 30	135.5	2.7	6822 17 US-10-282-122A-29931
Command line parameters:		c : 31	135	2.7	2643 9 US-09-350-874-16
-MDBL=frame_plus_p2n,model : DEVXplip -runat 16042005_115020_17247/app_query.fasta_1.1095		c : 32	135	2.7	2643 15 US-10-106-989-56
-Q : cgn2_1/USPTO_spool.D/US09671687/runat_16042005_115020_17247/app_query.fasta		c : 33	134.5	2.7	3103 9 US-09-764-868-118
-DB=Published Applications NA -OFTW=fastap -SUFFIX= rnpb -WINMATCH=0.1		c : 34	134.5	2.7	Sequence 542, App
-LOCOPCL=0 -LOCOPEXT=0 -UNITS=bis -END=1 -START=1 -DALIGN=300 -DOALIGN=45 -THR SCORE=opt -THR MAX=100		c : 35	134	2.7	Sequence 1329, App
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -LIST=0 -WAIT=0 -HEAPSIZE=500 -MINLEN=0		c : 36	134	2.7	Sequence 919, App
-MAXLEN=1000 -MAXLEN=1000 -OUTFILE=gn2_167 @runat 16042005_115020_17247		c : 37	133	2.7	2855 17 US-10-094-749-519
-NCPU=6 -ICPU=3 -NOMMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100		c : 38	132.5	2.6	3245 17 US-10-120-988-352
-LONGLOG -DEV TIMEOUT=30 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5		c : 39	132	2.6	1416 13 US-10-087-12-116
-FGAPOP=6 -FGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELEXT=7		c : 40	130	2.6	3338 19 US-10-491-213-65
Database :		c : 41	129.5	2.6	2676 17 US-10-276-774-450
Published_Applications_NA:*		c : 42	129.5	2.6	4839 18 US-10-363-829-121
1: /cgna_6/podata/1/pubpna/us07_pubcomb.seq:*		c : 43	129.5	2.6	10531 14 US-10-160-774-10
2: /cgna_6/podata/1/pubpna/us07_pubcomb.seq:*		c : 44	128.5	2.6	10759 17 US-10-210-172-49
3: /cgna_6/podata/1/pubpna/us08_pubcomb.seq:*		c : 45	128.5	2.6	2446 9 US-09-801-275-1
4: /cgna_6/podata/1/pubpna/us09_pubcomb.seq:*				Sequence 58, App1	
5: /cgna_6/podata/1/pubpna/us07_pubcomb.seq:*					
6: /cgna_6/podata/1/pubpna/pctig_pubcomb.seq:*					
7: /cgna_6/podata/1/pubpna/us08_pubcomb.seq:*					
8: /cgna_6/podata/1/pubpna/us08_pubcomb.seq:*					
9: /cgna_6/podata/1/pubpna/us09_pubcomb.seq:*					
10: /cgna_6/podata/1/pubpna/us09_pubcomb.seq:*					
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13: /cgna_6/podata/1/pubpna/us10_pubcomb.seq:*					
14: /cgna_6/podata/1/pubpna/us10_pubcomb.seq:*					
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16: /cgna_6/podata/1/pubpna/us10_pubcomb.seq:*					
17: /cgna_6/podata/1/pubpna/us10_pubcomb.seq:*					
18: /cgna_6/podata/1/pubpna/us10_pubcomb.seq:*					
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20: /cgna_6/podata/1/pubpna/us11_pubcomb.seq:*					
21: /cgna_6/podata/1/pubpna/us09_pubcomb.seq:*					
22: /cgna_6/podata/1/pubpna/us09_pubcomb.seq:*					

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGMENTS

RESULT 1
US-09-671-673-3
; Sequence 3, Application US/09851673
; Publication No. US20030165985A1
; GENERAL INFORMATION:
; APPLICANT: Derry, Jonathan
; APPLICANT: Fanallow, William
; APPLICANT: Dougall, William
; TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS OR ANTAGONISTS OF CD40 SIGNALING
; FILE REFERENCE: 3198
; CURRENT APPLICATION NUMBER: US/09/851,673
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 3
; LENGTH: 5371
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: NAME/KEY: CDS

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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:18:59 ; Search time 22 Seconds
(without alignments)
4150.441 Million cell updates/sec

Title: US-09-671-687A-3
Perfect score: 5034
Sequence: 1 MSSGILWSQBRVTKTSPPYWEERI.....RLLCDAYMCMYQSPPTMSLYK 949

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96226763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%, Maximum Match 100%
Listing First 45 summaries

Database : PIR_79.*
1: pir1:/*
2: pir2:/*
3: pir3:/*
4: pir4:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	613.5	F40F12.5	1021	2	F88568	protein F40F12.5 [protein F40F12.5]
2	590.5	11.7	727	2	A43334	microtubule-vesicle
3	151.1	3.0	1392	2	A43335	resin - human
4	151.0	3.0	1427	2	S22695	cycloplasmic linker
5	149.5	3.0	1046	2	T42734	cycloplasmic linker
6	149.4	3.0	1046	2	T42720	hemagglutinin/hemo
7	133.5	2.7	2273	2	T09033	SSV7 protein homolog
8	131.0	2.6	717	2	S38177	Kinesin-73 - fruit
9	124.5	2.5	1921	2	T13827	5-methyltetrahydro
10	124.5	2.5	1146	2	F83853	large repetitive p
11	124.4	2.5	3624	2	AD0835	BNT1 protein - yeast
12	122.5	2.4	1953	2	S63244	hypothetical prote
13	122.4	2.4	1791	2	T02345	hypothetical prote
14	121.1	2.4	1498	2	B86312	early nodulin bind
15	121.1	2.4	1641	2	T10935	hypothetical prote
16	120.0	2.4	499	2	S56265	probable transcript
17	119.9	2.4	662	2	T18233	CLIA protein - rat
18	118.5	2.4	1466	2	T17138	latrophilin-1, bra
19	118.5	2.4	1467	2	T18411	CLIBA protein - rat
20	118.5	2.4	1471	2	T17149	latrophilin-1, bra
21	118.5	2.4	1472	2	T18413	CLIBB protein - rat
22	118.5	2.4	1510	2	T17145	CLIBB protein - rat
23	118.5	2.4	1515	2	T17156	hypothetical prote
24	116.5	2.3	825	2	T47164	hypothetical prote
25	116.5	2.3	2484	2	T26216	hypothetical prote
26	116.5	2.3	2607	2	T26215	hypothetical prote
27	115.5	2.3	514	2	T25509	microtubule-associ
28	115.5	2.3	670	2	T28446	transcription fact
29	115.5	2.3	673	2	S35335	

ALIGNMENTS

RESULT 1							
P88568	protein F40F12.5 [imported] - Caenorhabditis elegans						
C;Species: Caenorhabditis elegans							
C;Date: 10-May-2001 #sequence_revision 10-May-2001							
C;Accession: F88568							
R;Anonymous, The C. elegans Sequencing Consortium.							
Science 282, 2012/2018, 1998							
A;Title: Genome sequence of the nematode <i>C. elegans</i> : a platform for investigating biology							
A;Reference number: A75000: PMID:9909613; PMID:9851916							
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/							
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an							
A;Accession: F88568							
A;Status: preliminary							
A;Molecule type: DNA							
A;Cross-references: GB:chr_III; PIDN:CAA82939.1; PID:93877002; GSPDB:GN00021; CESP:F40F							
C;Genetics:							
A;Gene: F40F12.5							
A;Map position: 3							
Query Match	256	Best Local Similarity	37.7%	Score	613.5;	DB	Length 1021;
Matches	256	Conservative	154	Pred. No.	4.6e-34;	Mismatches	357;
Qy	103	TNCBFRSLF-----KQENRILSKGLQIDIVGCPVQLRSGEKBPKPGVVRFRGPLLAAERTV	157	Qy	103	TNCBFRSLF-----KQENRILSKGLQIDIVGCPVQLRSGEKBPKPGVVRFRGPLLAAERTV	157
Dy	43	TOSEKNSNLNTSNTSNSNRNLNQNPNPGT-----	73	Dy	43	TOSEKNSNLNTSNTSNSNRNLNQNPNPGT-----	73
Qy	158	SGIFFGVILLEEEGRGGQTDGYYQQKGQLQFCQDCCGFVALDKLIEDDDTALE-----	211	Qy	158	SGIFFGVILLEEEGRGGQTDGYYQQKGQLQFCQDCCGFVALDKLIEDDDTALE-----	211
Dy	74	--LDGFPLINEASGGFLD-----DQI-----VDVSDYSRDTETKLDRNRNSP	115	Dy	74	--LDGFPLINEASGGFLD-----DQI-----VDVSDYSRDTETKLDRNRNSP	115
Qy	212	-----SDYAGPGDTMQVELPPLEI-----NSRVS	235	Qy	212	-----SDYAGPGDTMQVELPPLEI-----NSRVS	235
Dy	116	ELIVALLORKVGIRFSNYGRBEEPCVIEPQGTMYREADDWKMSKELKWFTSKS2AS	175	Dy	116	ELIVALLORKVGIRFSNYGRBEEPCVIEPQGTMYREADDWKMSKELKWFTSKS2AS	175
Qy	236	--LKGG----ETIESGTVIFC-----DVLP-GKEISLGIFYGVDMNPIGNWDGRFPDCV	281	Qy	236	--LKGG----ETIESGTVIFC-----DVLP-GKEISLGIFYGVDMNPIGNWDGRFPDCV	281
Dy	176	SHURDGLAMPMEELDC-TPLICAMITRSVMARINODQAIHLJAVSVERI-----EV	226	Dy	176	SHURDGLAMPMEELDC-TPLICAMITRSVMARINODQAIHLJAVSVERI-----EV	226
Qy	282	LCSFAVESTILLHINDIIPESY--TOERRPPKLAFMSSRGVGDKG-----	324	Qy	282	LCSFAVESTILLHINDIIPESY--TOERRPPKLAFMSSRGVGDKG-----	324
Dy	227	YQNFEWENFILNUKIGDSVSEVEDMRVPAKSVIGERPEASGIVNVDPDGNTSOMP	286	Dy	227	YQNFEWENFILNUKIGDSVSEVEDMRVPAKSVIGERPEASGIVNVDPDGNTSOMP	286
Qy	325	-----SSSHNKE-----KATGSTS-DPGNRRSELFLYN-----GSSVDS--	358	Qy	325	-----SSSHNKE-----KATGSTS-DPGNRRSELFLYN-----GSSVDS--	358
Dy	287	SSNOSSYSSSHDRILANQFDTNWAFMSGSSVAFN--GRLYSPNQHMMPKGCGVSALEY	344	Dy	287	SSNOSSYSSSHDRILANQFDTNWAFMSGSSVAFN--GRLYSPNQHMMPKGCGVSALEY	344
Qy	359	-----QPSKSKNTWYIDEVAEDPAKSLLTIS	385	Qy	359	-----QPSKSKNTWYIDEVAEDPAKSLLTIS	385
Dy	345	DNRLLVQYSGDDEOYRSAPKAPRERIIPVSRQPEIQRN-----SRSMKPE	393	Dy	345	DNRLLVQYSGDDEOYRSAPKAPRERIIPVSRQPEIQRN-----SRSMKPE	393

Result No.	Score	Query	Match	Length	DB ID	Description	SUMMARIES
1	4494	EST:*	gb est1:*	89.3	AF161542	AF161542 Homo sapi	
2	4313	EST:*	gb est2:*	85.7	AY406374	AY406374 Homo sapi	
3	4102	EST:*	gb htc:*	81.5	AY406376	AY406376 Mus muscu	
4	3768	EST:*	gb est3:*	74.9	AY406375	AY406375 Pan trogl	
5	2952	EST:*	gb est4:*	58.6	AK039054	AK039054 Mus muscu	
6	2739	EST:*	gb est5:*	55.0	BC028885	BC028885 Mus muscu	
7	15725	EST:*	gb g881:*	51.37	AY433523	AY433523 AGENCOURT	
8	15705	EST:*	gb g882:*	31.2	BM457960	BM457960 AGENCOURT	
9	14595	EST:*		29.0	AK042764	AK042764 Mus muscu	

Scoring table: BLASTMS52						
Gapop 10.0 , Gapext 0.5						
Searched: 1612378 seqs, 512079187 residues						
Total number of hits satisfying chosen parameters: 1612378						
Minimum DB seq length: 0						
Maximum DB seq length: 2000000000						
Post-processing: Minimum Match 0%						
Database : UniProt 03-* 1: uniprot_trembl: 2: uniprot_trembl: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the result being printed.						
SUMMARIES						
Result No.	Score	Query	Match	Length	DB ID	Description
1	4971.5	98.8	956	1	CYLD_HUMAN	Q9ncg7 homo sapien
2	4718.5	93.7	952	1	CYLD_MOUSE	Q80tg2 mus musculus
3	4712	93.6	953	2	Q66H52	Q66H52 rattus norvegicus
4	1207	24.0	778	2	Q7Q14	Q7Q14 anopheles gambiae
5	1136.5	22.6	551	2	Q8IPC3	Q8IPC3 drosophila melanogaster
6	1136.5	22.6	639	2	Q8IPC5	Q8IPC5 drosophila melanogaster
7	1114	22.5	550	2	Q8IPCA	Q8IPCA drosophila melanogaster
8	1132	22.5	639	2	Q8SYF0	Q8SYF0 drosophila melanogaster
9	1092.5	21.7	454	2	Q6TXK6	Q6TXK6 rattus norvegicus
10	856	17.0	517	2	Q9VLO4	Q9VLO4 drosophila melanogaster
11	619	12.3	1144	2	Q7JMS4	Q7JMS4 caenorhabditis elegans
12	183.5	3.6	258	2	Q7PJA3	Q7PJA3 anopheles gambiae
13	153	3.0	528	2	Q6ba87	Q6ba87 debaryomyces hansenii
14	151	3.0	653	2	Q6PSZ9	Q6PSZ9 homo sapien
15	151	3.0	1427	1	REST_HUMAN	P3022 homo sapien
16	149.5	3.0	1046	2	Q5L516	Q5L516 rattus norvegicus
17	149	3.0	1046	2	Q9Z0H8	Q9Z0H8 mus musculus
18	147.5	2.9	449	2	Q86WU4	Q86WU4 homo sapien
19	146	2.9	350	2	Q6PIA3	Q6PIA3 homo sapien
20	145	2.9	547	2	Q96DZ5	Q96DZ5 homo sapien
21	145	2.9	1556	2	Q9VRP1	Q9VRP1 drosophila melanogaster
22	143.5	2.9	495	2	Q6FM69	Q6FM69 candida glabrata
23	143.5	2.9	1047	2	Q9EPB1	Q9EPB1 mus musculus
24	143	2.8	547	2	Q8WWL1	Q8WWL1 homo sapien
25	142.5	2.8	1606	2	Q7PVQ8	Q7PVQ8 anopheles gambiae
26	142	2.8	1012	2	Q7TST9	Q7TST9 mus musculus
27	141	2.8	1012	2	Q8CHU1	Q8CHU1 mus musculus
28	141	2.8	1429	2	Q6DPB6	Q6DPB6 xenopus laevis
29	140.5	2.8	429	2	Q9EBC9	Q9EBC9 homo sapien
30	140	2.8	924	2	Q7VDY2	Q7VDY2 prochlorococcus marinus
31	139.5	2.8	1921	2	Q86BR0	Q86BR0 drosophila melanogaster

RESULT 1 CYLD_HUMAN						
ID	CYLD_HUMAN	STANDARD	PRY;	PRY;	956 AA.	.
AC	Q94934; QTL3N6; Q96FB0; Q9NZX9;					
DT	25-OCT-2004 (Rel. 45, Created)					
DT	25-OCT-2004 (Rel. 45, Last sequence update)					
DT	25-OCT-2004 (Rel. 45, Last annotation update)					
DE	Probable ubiquitin carboxyl-terminal hydrolase CYLD (EC 3.1.2.15)					
DE	(Ubiquitin thioesterase CYLD) (Ubiquitin-specific processing protease CYLD) (Deubiquitinating enzyme CYLD) (HSPC057).					
GN	Name=CYLD; Synonyms=CYLD1, KIAA0499;					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OC	NCB_ TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A. (ISOFORM 1), DISEASE, AND TISSUE SPECIFICITY.					
RX	Medline=0296617; PubMed=1035622; DOI=10.1038/76006;					
RA	Bigrell G.R., Brown C., Biggs P.J., Lakhani S.R., Jones C., Hansen J., Blair E., Hofmann B., Siebert R., Turner G., Evans D.G., Schanderman-Stumpel C., Van Den Ouweland A., Hallely D., Delpech B., Cleveland M.G., Leigh I., Leisti J., Rasmussen S., Wallace M.R., Penske C., Banerjee P., Oiso N., Chagger R., Merrett S., Leonard N., Huber M., Hoh D., Chapman P., Burn J., Swift S., Smith A., Ashworth A., Stratton M.R.; Gen.					
RA	"Identification of the familial cylindromatosis tumor suppressor gene." Nat. Genet. 25:160-165 (2000). [2]					
RA	Medline=9915230; PubMed=10048485;					
RP	SEQUENCE=brain. TISSUE=brain: TISSUE=brain: TISSUE=brain:					
RC	Nagae T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosewa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.", DNA Res. 5:355-364 (1998). [3]					
RP	SEQUENCE FROM N.A. (ISOFORM 2). TISSUE=uterus; TISSUE=uterus; TISSUE=uterus;					
RC	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altchek S.P., Zeeberg B.B., Buetow K.H., Schaefer C.P., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J., Boisvert S.A., McEwan P.J., McKernan K.J., Malek A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Gibbs R.A., Fahey J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,					